WHAT IS CLAIMED IS:

1. An isolated polynucleotide from Coryneform bacteria, comprising a polynucleotide sequence which codes for ccpA1 gene, which comprises:

a) a polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2, or

b) a polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2, or

c) a polynucleotide which is complementary to the polynucleotides of a) or b), or

d) a polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b), or c), or a mixture thereof.

2. The isolated polynucleotide of Claim 1, wherein the coded polypeptide therefor exhibits activity of catabolite control protein ccpA1.

3. The isolated polynucleotide of Claim 1, wherein the polynucleotide is a recombinant DNA which is capable of replication in Coryneform bacteria.

4. The isolated polynucleotide of Claim 1, wherein the polynucleotide is an RNA.

5. The isolated polynucleotide of Claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

6. The recombinant DNA of Claim 3, which is capable of replication, comprising

(i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequences complementary to sequences (i) or (ii), and optionally

(iv) sense mutations of neutral function in (i).

7. The isolated polynucleotide sequence of Claim 3, which codes for a polypeptide which comprises the amino acid sequence in SEQ ID No. 2.

8. A Coryneform bacterium in which a ccpA1 gene thereof is attenuated.

9. The Coryneform bacterium of Claim 8, wherein the ccpA1 gene thereof is eliminated.

10. *Escherichia coli* strain Top10F/pCR2.1ccpA1int as DSM 13673 deposited at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (German Collection of Microorganisms and Cell Cultures), Braunschweig, Germany.

11. Vector pCR2.1ccpA1int, which

11.1. carries an internal fragment of the ccpA1 gene 362 bp in size,

11.2. the restriction map of which is reproduced in figure 1, and

11.3. is deposited in the *E. coli* strain Top10/pCR2.1ccpA1int under no. DSM 13673 at the Deutsche Sammlung für Mikroorganismen und Zellenkulturen (German Collection of Microorganisms and Cell Cultures).

12. A process for preparing L-amino acids, which comprises the steps of:

a) fermenting bacteria which produce a desired L-amino acid and in which at least a ccpA1 gene thereof is attenuated;

b) concentrating the desired product L-amino acid in the medium or in the cells of the bacteria; and

c) isolating the product L-amino acid.

13. The process of Claim 12, wherein the fermenting bacteria in which further genes of a biosynthetic pathway of the desired L-amino acid are enhanced.

14. The process of Claim 12, wherein metabolic pathways of the fermenting bacteria which reduce formation of the desired L-amino acid have been at least partly eliminated.

15. The process of Claim 12, wherein the fermenting bacteria exhibit a decreased expression of the polynucleotide(s) coding for the ccpA1 gene.

16. The process of Claim 15, wherein the expression of the polynucleotide(s) which code for the ccpA1 gene is eliminated.

17. The process of Claim 12, wherein the fermenting bacteria comprise one or more of the following genes:

17.1 the dapA gene which codes for dihydrodipicolinate synthase,

17.2 the eno gene which codes for enolase,

17.3 the zwf gene which codes for the zwf gene product,

17.4 the pyc gene which codes for pyruvate carboxylase,

17.5 the lysE gene which codes for lysine export,

17.6 at the same time the dapD gene which codes for tetradihydrodipicolinate succinylase,

17.7 at the same time the dapE gene which codes for succinyl diamino-pimelate desuccinylase,

17.8 at the same time the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

17.9 at the same time the mqo gene which codes for malate:quinone oxidoreductase,

17.10 the lysC gene which codes for a feed back resistant aspartate kinase, or

17.11 the zwa1 gene which codes for the Zwa1 protein which one or more genes are

18. The process of Claim 12, wherein for the preparation of L-amino acids, in particular L-lysine, bacteria in which at the same time one or more of the genes chosen from the group consisting of

18.1 the dapA gene which codes for dihydrodipicolinate synthase,

18.2 the eno gene which codes for enolase,

18.3 the zwf gene which codes for the zwf gene product,

18.4 the pyc gene which codes for pyruvate carboxylase,

18.5 the lysE gene which codes for lysine export,

18.6 at the same time the dapD gene which codes for tetradihydrodipicolinate succinylase,

18.7 at the same time the dapE gene which codes for succinyl diamino-pimelate desuccinylase,

18.8 at the same time the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

18.9 at the same time the mqo gene which codes for malate:quinone oxidoreductase,

18.10 the lysC gene which codes for a feed back resistant aspartate kinase, or

18.11 the zwa1 gene which codes for the Zwa1 protein which one or more genes are enhanced.

19. The process of Claim 17, wherein said one or more genes are over-expressed.

20. The process of Claim 17, wherein at the same time said one or more genes are over-expressed.

21. The process of Claim 12, wherein microorganisms of the genus Corynebacterium are employed.

22. The process of Claim 21, wherein said microorganisms are *Corynebacterium glutamicum*.

23. The process of Claim 22, wherein said microorganisms are selected from the group consisting of

Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum FERM-P 1709
Corynebacterium glutamicum FERM-P 6463
Corynebacterium glutamicum FERM-P 6464
Corynebacterium glutamicum DM 58-1
Corynebacterium glutamicum DG 52-5
Corynebacterium glutamicum DJM 5715
Corynebacterium glutamicum DJM 12866

24. A process for identifying RNA, cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes which code for the catabolite control protein ccpA1 or have a structural similarity with the sequence of the ccpA1 gene, which comprises effecting said identification using the polynucleotide sequences of Claim 1, as hybridization probes.

25. The process of Claim 24, wherein the hybridization is carried out under a stringency corresponding to at most 2x SSC.